SEQUENCE LISTING

<110> Connelly, Mariah
Brody, Howard

<120> Methods For Producing Biological Substances In Enzyme-Deficient Mutants Of Aspergillus Niger

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<140> 10/815,495
<141> 2004-03-31

<150> 60/459,902
<151> 2003-03-31

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Gln Leu Met Pro Glu Val Met Pro Ser Ser Phe Pro Asp Gly Ile Leu
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Asn Gly Met Pro Val Thr Gly Leu Ala Ala Tyr Arg Ser Ala Thr Leu
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Ser Ser Asn Thr Arg Asp Asp Asn Leu Gln Arg Trp Phe Ser Ser Cys
645 650 655

Pro Trp Ala Glu Leu Lys Pro Arg Thr Pro
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<213> Aspergillus niger

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<213> Aspergillus niger

<400> 16
tcagccacac ctgcaaaggc 20

<210> 17
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<213> Aspergillus niger

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<223> n=a,c,g or t

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gccatgcttg gaggatagca accgacaaca tcacatcaag ctctcccttc tctgaacaat 180

aaaccccaca gaaggcattt atgatggtcg cgtggtggtc tctatttctg tacggccttc 240

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cggatcaggt gtgttgttac ctactagctt tcagaaagag gaatgtaaac tgacttgata 420

tagaaatact gtggtggaac atggcagggc atcatcgaca aggtaaattg ccccttttatc 480

aaaaaaaaag aaggaaaagc agaagaaaaa taaaataaaa agaactctag tcctaaccat 540

cacatagttg gactatatcc agggaatggg cttcacagcc atctggatca cccccgttac 600

agcccagctg ccccagacca ccgcatatgg agatgcctac catggctact ggcagcagga 660

tatgtaagtc gatttcttta aatatctacc tgtcatcttt tacatcaata tgaactaact 720

tgatggtttt agatactctc tgaacgaaaa ctacggcact gcagatgact tgaaggcgct 780

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cggcctccgt atcgacacag taaaacacgt ccagaaggac ttctggcccg ggtacaacaa 1260

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<212> PRT
<213> Aspergillus niger

<400> 18

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Tyr Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr
35 40 45

Ala Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln
50 55 60

Gly Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65 70 75 80

Ile Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr
85 90 95

Gly Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn
100 105 110

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Glu Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu
        115                 120                 125

His Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met
    130                 135                 140

Gly Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro
145                 150                 155                 160

Phe Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr
                165                 170                 175

Glu Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val
            180                 185                 190

Ser Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp
        195                 200                 205

Tyr Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu
    210                 215                 220

Arg Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr
225                 230                 235                 240

Asn Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp
                245                 250                 255

Pro Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn
            260                 265                 270

Tyr Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly
        275                 280                 285

Ser Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys
    290                 295                 300

Pro Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro
305                 310                 315                 320

Arg Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala
                325                 330                 335
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Ala Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln
340 345 350

Glu Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr
355 360 365

Trp Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala
370 375 380

Ser Arg Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe
385 390 395 400

Val Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Pro
405 410 415

Met Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn
420 425 430

Lys Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly
435 440 445

Tyr Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val
450 455 460

Thr Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu
465 470 475 480

Pro Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys
485 490 495

Ser Ser Ser

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<212> DNA
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<210> 20
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<213> Aspergillus niger

<400> 20
cactgtaatc gactgagcta c 21

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gccatgcttg gaggatagca accgacaaca tcacatcaag ctctcccttc tctgaacaat 180

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tagaaatact gtggtggaac atggcagggc atcatcgaca aggtaaattg ccccttttatc 480

aaaaaaaaag aaggaaaagc agaagaaaaa taaaataaaa agaactctag tcctaaccat 540

cacatagttg gactatatcc agggaatggg cttcacagcc atctggatca cccccgttac 600

agcccagctg ccccagacca ccgcatatgg agatgcctac catggctact ggcagcagga 660

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gattcgtgac ctacaaggta agcacaacct ctaagcatac cctaatggcc tatcttcaga 1920

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<212> PRT
<213> Aspergillus niger

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Tyr Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr
        35                  40                  45

Ala Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln
    50                  55                  60

Gly Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala
65                  70                  75                  80

Ile Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr
                85                  90                  95

Gly Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn
            100                 105                 110

Glu Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu
        115                 120                 125

His Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met
    130                 135                 140

Gly Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro
145                 150                 155                 160

Phe Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr
                165                 170                 175

Glu Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val
            180                 185                 190

Ser Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp
        195                 200                 205

Tyr Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu
    210                 215                 220
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Arg Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr
225                 230                 235                 240

Asn Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp
                245                 250                 255

Pro Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn
            260                 265                 270

Tyr Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly
        275                 280                 285

Ser Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys
    290                 295                 300

Pro Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro
305                 310                 315                 320

Arg Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala
                325                 330                 335

Ala Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln
            340                 345                 350

Glu Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr
        355                 360                 365

Trp Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala
    370                 375                 380

Ser Arg Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe
385                 390                 395                 400

Val Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Pro
                405                 410                 415

Met Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn
            420                 425                 430

Lys Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly
        435                 440                 445
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Tyr Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val
450 455 460

Thr Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu
465 470 475 480

Pro Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys
485 490 495

Tyr Gly

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<212> DNA
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accatttttct tttcttttct cggcgctggg atggtggcca agaaaattga atggcaatgg 780

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gtcttgmtga ttca 3494

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<211> 341
<212> PRT
<213> Aspergillus niger

<400> 24

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Thr Ile Thr Ile Thr Val Glu Gln Asp Gly Ile Tyr Glu Ile Asn Gly
20 25 30

Ala Arg Gln Glu Pro Val Val Asn Leu Asn Met Val Thr Gly Ala Ser
35 40 45

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Lys Leu Arg Lys Gln Leu Arg Glu Thr Asn Glu Leu Leu Val Cys Pro
     50                  55                  60

Gly Val Tyr Asp Gly Leu Ser Ala Arg Ile Ala Ile Asn Leu Gly Phe
65                  70                  75                  80

Lys Gly Met Tyr Met Thr Gly Ala Gly Thr Thr Ala Ser Arg Leu Gly
                85                  90                  95

Met Ala Asp Leu Gly Leu Ala His Ile Tyr Asp Met Lys Thr Asn Ala
            100                 105                 110

Glu Met Ile Ala Asn Leu Asp Pro Tyr Gly Pro Pro Leu Ile Ala Asp
        115                 120                 125

Met Asp Thr Gly Tyr Gly Gly Pro Leu Met Val Ala Arg Ser Val Gln
    130                 135                 140

Gln Tyr Ile Gln Ala Gly Val Ala Gly Phe His Ile Glu Asp Gln Ile
145                 150                 155                 160

Gln Asn Lys Arg Cys Gly His Leu Ala Gly Lys Arg Val Val Thr Met
                165                 170                 175

Asp Glu Tyr Leu Thr Arg Ile Arg Ala Ala Lys Leu Thr Lys Asp Arg
            180                 185                 190

Leu Arg Ser Asp Ile Val Leu Ile Ala Arg Thr Asp Ala Leu Gln Gln
        195                 200                 205

His Gly Tyr Asp Glu Cys Ile Arg Arg Leu Lys Ala Ala Arg Asp Leu
    210                 215                 220

Gly Ala Asp Val Gly Leu Leu Glu Gly Phe Thr Ser Lys Glu Met Ala
225                 230                 235                 240

Arg Arg Cys Val Gln Asp Leu Ala Pro Trp Pro Leu Leu Leu Asn Met
                245                 250                 255

Val Glu Asn Gly Ala Gly Pro Val Ile Ser Val Asp Glu Ala Arg Glu
            260                 265                 270
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Met Gly Phe Arg Ile Met Ile Phe Ser Phe Ala Cys Ile Thr Pro Ala
275 280 285

Tyr Met Gly Ile Thr Ala Ala Leu Glu Arg Leu Lys Lys Asp Gly Val
290 295 300

Val Gly Leu Pro Glu Gly Met Gly Pro Lys Lys Leu Phe Glu Val Cys
305 310 315 320

Gly Leu Met Asp Ser Val Arg Val Asp Thr Glu Ala Gly Gly Asp Gly
325 330 335

Phe Ala Asn Gly Val
340

<210> 25
<211> 21
<212> DNA
<213> Aspergillus niger

<400> 25
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<210> 26
<211> 21
<212> DNA
<213> Aspergillus niger

<400> 26
gcaccgttct ccaccatgtt g 21

<210> 27
<211> 1389
<212> DNA
<213> Candida antarctica

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cccttctaca cgacgccatc caacatcggc acgtttgcca agggccaggt gatccaatct 180

cgcaaggtgc ccacggacat cggcaacgcc aacaacgctg cgtcgttcca gctgcagtac 240

cgcaccacca atacgcagaa cgaggcggtg gccgacgtgg ccaccgtgtg gatcccggcc 300

aagcccgctt cgccgcccaa gatcttttcg taccaggtct acgaggatgc cacggcgctc 360

gactgtgctc cgagctacag ctacctcact ggattggacc agccgaacaa ggtgacggcg 420

gtgctcgaca cgcccatcat catcggctgg gcgctgcagc agggctacta cgtcgtctcg 480

tccgaccacg aaggcttcaa agccgccttc atcgctggct acgaagaggg catggctatc 540

ctcgacggca tccgcgcgct caagaactac cagaacctgc catccgacag caaggtcgct 600

cttgagggct acagtggcgg agctcacgcc accgtgtggg cgacttcgct tgctgaatcg 660

tacgcgcccg agctcaacat tgtcggtgct tcgcacggcg gcacgcccgt gagcgccaag 720

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tttatcaagc aagccttcga cggcaccaca cccaaggtga tctgcggcac tcccatccct 1260

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<210> 28
<211> 462
<212> PRT
<213> Candida antarctica

<220>
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<223> X=Xaa

<400> 28

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Ala Ala Val Leu Ala Ala Pro Ala Ala Glu Thr Leu Asp Arg Arg Ala
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Ala Leu Pro Asn Pro Tyr Asp Asp Pro Phe Tyr Thr Thr Pro Ser Asn
        35                  40                  45

Ile Gly Thr Phe Ala Lys Gly Gln Val Ile Gln Ser Arg Lys Val Pro
    50                  55                  60

Thr Asp Ile Gly Asn Ala Asn Asn Ala Ala Ser Phe Gln Leu Gln Tyr
65                  70                  75                  80

Arg Thr Thr Asn Thr Gln Asn Glu Ala Val Ala Asp Val Ala Thr Val
                85                  90                  95

Trp Ile Pro Ala Lys Pro Ala Ser Pro Pro Lys Ile Phe Ser Tyr Gln
            100                 105                 110

Val Tyr Glu Asp Ala Thr Ala Leu Asp Cys Ala Pro Ser Tyr Ser Tyr
        115                 120                 125

Leu Thr Gly Leu Asp Gln Pro Asn Lys Val Thr Ala Val Leu Asp Thr
    130                 135                 140

Pro Ile Ile Ile Gly Trp Ala Leu Gln Gln Gly Tyr Tyr Val Val Ser
145                 150                 155                 160

Ser Asp His Glu Gly Phe Lys Ala Ala Phe Ile Ala Gly Tyr Glu Glu
                165                 170                 175

Gly Met Ala Ile Leu Asp Gly Ile Arg Ala Leu Lys Asn Tyr Gln Asn
            180                 185                 190

Leu Pro Ser Asp Ser Lys Val Ala Leu Glu Gly Tyr Ser Gly Gly Ala
        195                 200                 205

His Ala Thr Val Trp Ala Thr Ser Leu Ala Glu Ser Tyr Ala Pro Glu
    210                 215                 220

Leu Asn Ile Val Gly Ala Ser His Gly Gly Thr Pro Val Ser Ala Lys
225                 230                 235                 240

Asp Thr Phe Thr Phe Leu Asn Gly Gly Pro Phe Ala Gly Phe Ala Leu
                245                 250                 255
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Ala Gly Val Ser Gly Leu Ser Leu Ala His Pro Asp Met Glu Ser Phe
            260                 265                 270

Ile Glu Ala Arg Leu Asn Ala Lys Gly Gln Arg Thr Leu Lys Gln Ile
        275                 280                 285

Arg Gly Arg Gly Phe Cys Leu Pro Gln Val Val Leu Thr Tyr Pro Phe
    290                 295                 300

Leu Asn Val Phe Ser Leu Val Asn Asp Thr Asn Leu Leu Asn Glu Ala
305                 310                 315                 320

Pro Ile Ala Ser Ile Leu Lys Gln Glu Thr Val Val Gln Ala Glu Ala
                325                 330                 335

Ser Tyr Thr Val Ser Val Pro Lys Phe Pro Arg Phe Ile Trp His Ala
            340                 345                 350

Ile Pro Asp Glu Ile Val Pro Tyr Gln Pro Ala Ala Thr Tyr Val Lys
        355                 360                 365

Glu Gln Cys Ala Lys Gly Ala Asn Ile Asn Phe Ser Pro Tyr Pro Ile
    370                 375                 380

Ala Glu His Leu Thr Ala Glu Ile Phe Gly Leu Val Pro Ser Leu Trp
385                 390                 395                 400

Phe Ile Lys Gln Ala Phe Asp Gly Thr Thr Pro Lys Val Ile Cys Gly
                405                 410                 415

Thr Pro Ile Pro Ala Ile Ala Gly Ile Thr Thr Pro Ser Ala Asp Gln
            420                 425                 430

Val Leu Gly Ser Asp Leu Ala Asn Gln Leu Arg Ser Leu Asp Gly Lys
        435                 440                 445

Gln Ser Ala Phe Gly Lys Pro Phe Gly Pro Ile Thr Pro Pro
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<211> 2794

<212> DNA
<213> Scytalidum thermophilum

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gcttgagttt ggggacatac ggagtacctt actgacgcgc tgaaccactc caggttcccg 420

aaagggcggt ccatgctcga ggcgctggag cacacgggac cttcacgagt tacgccgact 480

ggagtaacat caccgcggcg tcctttctga acgccactgg aaagcagacg ccggtgtttg 540

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gtttcgcgac gcggtttgta agttttgttg tgtttcattc gttccggtct gtagaggagg 660

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ctaacttgcg taggatatcg tcggaaacaa catcccggta ttcttcattc aagatgcaat 840

ccagttccct gaccttatcc actcggtcaa gccgcgtccc gacaacgaga ttccccaagc 900

ggcgacggct catgattcag cttgggactt cttcagccag cagccaagca ccatggtaag 960

caatggacca aggagccgca cctggggtga catgccaggg agtacacaag gcgttccgat 1020

gaccctcgtg tgaccaaggc agtacaacac tccacggagg actcgaagag attcggcaat 1080

atggaacaca gaactgacag gatggtagca cacgttgttc tgggccatgt ccggccacgg 1140

aatccctcgc agctaccgcc atatggtacg tttgcctggc tgagatgacc gtgaatccat 1200

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gatgctattg agtccgggaa cggaccagaa tgggatgtct gcgtccagat tgtcgatgag 1440

tcccaggcgc aagcctttgg cttcgacttg ctggacccga caaagatcat ccccgaggag 1500

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aacagtggtt atccgcggca agccaaccaa aatgccggac gcggattctt cacagcgcct 1920

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tcgcagcccc gtctcttctt caactccctc actcccgtcg aacaacagtt cctcgtcaac 2040

gccatgcgct tcgaaatcag ccttgtgaag tcggaagaag tcaagaagaa cgtgctcacc 2100

cagctcaacc gcgtcagcca tgacgtggcc gtgcgcgtgg ccgccgctat cggcctcggc 2160

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<210> 30
<211> 717
<212> PRT
<213> Scytalidium thermophilum

<400> 30

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Ala Gln Ala Thr Cys Pro Phe Ala Asp Pro Ala Ala Leu Tyr Ser Arg
20 25 30

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Gln Asp Thr Thr Ser Gly Gln Ser Pro Leu Ala Ala Tyr Glu Val Asp
        35                  40                  45

Asp Ser Thr Gly Tyr Leu Thr Ser Asp Val Gly Gly Pro Ile Gln Asp
    50                  55                  60

Gln Thr Ser Leu Lys Ala Gly Ile Arg Gly Pro Thr Leu Leu Glu Asp
65                  70                  75                  80

Phe Met Phe Arg Gln Lys Ile Gln His Phe Asp His Glu Arg Val Pro
                85                  90                  95

Glu Arg Ala Val His Ala Arg Gly Ala Gly Ala His Gly Thr Phe Thr
            100                 105                 110

Ser Tyr Ala Asp Trp Ser Asn Ile Thr Ala Ala Ser Phe Leu Asn Ala
        115                 120                 125

Thr Gly Lys Gln Thr Pro Val Phe Val Arg Phe Ser Thr Val Ala Gly
    130                 135                 140

Ser Arg Gly Ser Ala Asp Thr Ala Arg Asp Val His Gly Phe Ala Thr
145                 150                 155                 160

Arg Phe Tyr Thr Asp Glu Gly Asn Phe Asp Ile Val Gly Asn Asn Ile
                165                 170                 175

Pro Val Phe Phe Ile Gln Asp Ala Ile Gln Phe Pro Asp Leu Ile His
            180                 185                 190

Ser Val Lys Pro Arg Pro Asp Asn Glu Ile Pro Gln Ala Ala Thr Ala
        195                 200                 205

His Asp Ser Ala Trp Asp Phe Phe Ser Gln Gln Pro Ser Thr Met His
    210                 215                 220

Thr Leu Phe Trp Ala Met Ser Gly His Gly Ile Pro Arg Ser Tyr Arg
225                 230                 235                 240

His Met Asp Gly Phe Gly Val His Thr Phe Arg Phe Val Lys Asp Asp
                245                 250                 255
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```
Gly Ser Ser Lys Leu Ile Lys Trp His Phe Lys Ser Arg Gln Gly Lys
            260                 265                 270

Ala Ser Leu Val Trp Glu Glu Ala Gln Val Leu Ser Gly Lys Asn Ala
        275                 280                 285

Asp Phe His Arg Gln Asp Leu Trp Asp Ala Ile Glu Ser Gly Asn Gly
    290                 295                 300

Pro Glu Trp Asp Val Cys Val Gln Ile Val Asp Glu Ser Gln Ala Gln
305                 310                 315                 320

Ala Phe Gly Phe Asp Leu Leu Asp Pro Thr Lys Ile Ile Pro Glu Glu
                325                 330                 335

Tyr Ala Pro Leu Thr Lys Leu Gly Leu Leu Lys Leu Asp Arg Asn Pro
            340                 345                 350

Thr Asn Tyr Phe Ala Glu Thr Glu Gln Val Met Phe Gln Pro Gly His
        355                 360                 365

Ile Val Arg Gly Ile Asp Phe Thr Glu Asp Pro Leu Leu Gln Gly Arg
    370                 375                 380

Leu Phe Ser Tyr Leu Asp Thr Gln Leu Asn Arg Asn Gly Gly Pro Asn
385                 390                 395                 400

Phe Glu Gln Leu Pro Ile Asn Met Pro Arg Val Pro Ile His Asn Asn
                405                 410                 415

Asn Arg Asp Gly Ala Gly Gln Met Phe Ile His Arg Asn Lys Tyr Pro
            420                 425                 430

Tyr Thr Pro Asn Thr Leu Asn Ser Gly Tyr Pro Arg Gln Ala Asn Gln
        435                 440                 445

Asn Ala Gly Arg Gly Phe Phe Thr Ala Pro Gly Arg Thr Ala Ser Gly
    450                 455                 460

Ala Leu Val Arg Glu Val Ser Pro Thr Phe Asn Asp His Trp Ser Gln
465                 470                 475                 480
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Pro Arg Leu Phe Phe Asn Ser Leu Thr Pro Val Glu Gln Gln Phe Leu
485 490 495

Val Asn Ala Met Arg Phe Glu Ile Ser Leu Val Lys Ser Glu Glu Val
500 505 510

Lys Lys Asn Val Leu Thr Gln Leu Asn Arg Val Ser His Asp Val Ala
515 520 525

Val Arg Val Ala Ala Ala Ile Gly Leu Gly Ala Pro Asp Ala Asp Asp
530 535 540

Thr Tyr Tyr His Asn Asn Lys Thr Ala Gly Val Ser Ile Val Gly Ser
545 550 555 560

Gly Pro Leu Pro Thr Ile Lys Thr Leu Arg Val Gly Ile Leu Ala Thr
565 570 575

Thr Ser Glu Ser Ser Ala Leu Asp Gln Ala Ala Gln Leu Arg Thr Arg
580 585 590

Leu Glu Lys Asp Gly Leu Val Val Thr Val Val Ala Glu Thr Leu Arg
595 600 605

Glu Gly Val Asp Gln Thr Tyr Ser Thr Ala Asp Ala Thr Gly Phe Asp
610 615 620

Gly Val Val Val Val Asp Gly Ala Ala Ala Leu Phe Ala Ser Thr Ala
625 630 635 640

Ser Ser Pro Leu Phe Pro Thr Gly Arg Pro Leu Gln Ile Phe Val Asp
645 650 655

Ala Tyr Arg Trp Gly Lys Pro Val Gly Val Cys Gly Gly Lys Ser Ser
660 665 670

Glu Val Leu Asp Ala Ala Asp Val Pro Glu Asp Gly Asp Gly Val Tyr
675 680 685

Ser Glu Glu Ser Val Asp Met Phe Val Glu Glu Phe Glu Lys Gly Leu
690 695 700

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Ala Thr Phe Arg Phe Thr Asp Arg Phe Ala Leu Asp Ser
705                 710                 715
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